

## **AMENDMENTS TO THE CLAIMS**

### **LISTING OF CLAIMS:**

Claim 1 (Currently amended). A process for preparing the production of a modified *Aspergillus* phytase with a specific activity improved over the specific activity of an unmodified *Aspergillus* phytase having a desired property improved over the property of the corresponding unmodified phytase which comprises:

(a) determining the three dimensional structure of the unmodified *Aspergillus* phytase and of a second phytase which has the improved specific activity desired property by aligning the amino acid sequences of said phytases with the amino acid sequence of a third phytase which is the phytase of *Aspergillus niger* and using the three dimensional structure of the phytase of *Aspergillus niger* as a template based on the alignment to determine said three dimensional structures;

(b) determining from the structures of step (a) the amino acids of the active sites of the unmodified *Aspergillus* phytase and of the second phytase having the improved specific activity desired property which active site provides the improved specific activity desired property and comparing the amino acids which form the active sites to identify which amino acids are different in the active site of the second phytase from the amino acids in the active site of the unmodified *Aspergillus* phytase;

(c) constructing a DNA sequence coding for the modified phytase by obtaining the DNA sequence of the unmodified *Aspergillus* phytase and changing the nucleotides coding for the active site which provides the improved specific activity desired property for said unmodified *Aspergillus* phytase so that at least one of the amino acids in the active site which provides the improved specific activity desired

Application No.: 10/776,104  
Amendment Dated: May 27, 2005  
Reply to Office Action of: February 10, 2005

~~property~~ is substituted by one of the amino acids which was identified as being different in step (b);

(d) integrating such a DNA sequence into a vector capable of expression in a suitable host cell; and

(e) transforming the suitable host cell by the DNA sequence of step (c) or the vector of step (d), growing said host cell under suitable growth conditions and isolating the modified phytase from the host cell or the culture medium.

Claims 2-4 (Cancelled).

Claim 5 (Currently amended). The process of claim 1 ~~[[4]]~~ wherein the unmodified phytase is a phytase from *Aspergillus fumigatus*.

Claim 6 (Currently amended). The process of claim 1 wherein the phytase with the improved specific activity ~~desired property~~ is of eukaryotic origin.

Claim 7 (Currently amended). The process of claim 6 wherein the phytase with the improved specific activity ~~desired property~~ is of fungal origin.

Claim 8 (Currently amended). The process of claim 7 wherein the phytase with the improved specific activity ~~desired property~~ is of *Aspergillus* origin.

Application No.: 10/776,104  
Amendment Dated: May 27, 2005  
Reply to Office Action of: February 10, 2005

Claim 9 (Currently amended). The process of claim 8 wherein the phytase with the improved specific activity ~~desired property~~ is a phytase from *Aspergillus terreus*.

Claim 10 (Currently amended). The process of claim 1 wherein the unmodified phytase is a phytase of *Aspergillus fumigatus* and the second phytase with the improved specific activity ~~desired property~~ is an the *Aspergillus niger* phytase.

Claim 11 (Currently amended). The process of claim 1 wherein the unmodified phytase is a phytase of *Aspergillus fumigatus* and the second phytase with the improved specific activity ~~desired property~~ is an the *Aspergillus terreus* phytase.

Claims 12- 24 (Cancelled).

Claim 25 (New). The process according to claim 1, wherein the DNA sequence encoding the modified *Aspergillus* phytase has been changed at a position corresponding to position 27 of the phytase of *Aspergillus niger* (SEQ ID NO:1) to an amino acid selected from the group consisting of Ala, Val, Leu, Ile, Thr, Gly, and Asn.

Claim 26 (New). A process according to claim 25, wherein the DNA sequence encodes at least one additional mutation selected from the group consisting of S66D, S140Y, D141G, A205E, Q274L, G277D, G277K, Y282H, and N340S.